SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
Chuntharapai, Anan
Kim, Kyung J.

(ii) TITLE OF INVENTION: Apo-2 Receptor

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Marschang, Diane L.
(B) REGISTRATION NUMBER: 35,600
(C) REFERENCE/DOCKET NUMBER: P1101R2

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650/225-5416
(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
20 25 30

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
35 40 45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
50 55 60

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
65 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
80 85 90

Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr
95 100 105

His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp
110 115 120

Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr
125 130 135

Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro
140 145 150

Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val
155 160 165

Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His
170 175 180

Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
185 190 195

Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
200 205 210

Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp
215 220 225

Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
230 235 240

Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val
245 250 255

Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly
260 265 270

Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
275 280 285

Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
290 295 300

Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
305 310 315

Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
320 325 330

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
335 340 345

Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
350 355 360

```
Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
                365                 370                 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
            380                 385                 390

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
        395                 400                 405

Ala Asp Ser Ala Xaa Ser
    410 411
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1799 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100

CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC  ATG GAA 145
                                           Met Glu
                                             1

CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184
Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
          5                  10                  15

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala
                20                  25

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262
Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val
     30                  35                  40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301
Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala
               45                  50

CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340
Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala
 55                  60                  65

GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379
Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
          70                  75                  80

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
                85                  90
```

```
TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457
Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His
     95                  100                 105

TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496
Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys
            110                 115

GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535
Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr
120                 125                 130

AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574
Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg
         135                 140                 145

GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613
Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
                150                 155

GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652
Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr
    160                 165                 170

CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691
Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly
            175                 180

ATC ATC ATA GGA GTC ACA GTT GCA GCC GTA GTC TTG ATT 730
Ile Ile Ile Gly Val Thr Val Ala Ala Val Val Leu Ile
185                 190                 195

GTG GCT GTG TTT GTT TGC AAG TCT TTA CTG TGG AAG AAA 769
Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
         200                 205                 210

GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT GGT GGT 808
Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly
                215                 220

GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT 847
Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro
    225                 230                 235

GGG GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC 886
Gly Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile
            240                 245

TTG CAG CCC ACC CAG GTC CCT GAG CAG GAA ATG GAA GTC 925
Leu Gln Pro Thr Gln Val Pro Glu Gln Glu Met Glu Val
250                 255                 260

CAG GAG CCA GCA GAG CCA ACA GGT GTC AAC ATG TTG TCC 964
Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
         265                 270                 275

CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT 1003
Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
                280                 285
```

```
GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT 1042
Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
    290                 295                 300

GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081
Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp
            305                 310

GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120
Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro
315                 320                 325

CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
        330                 335                 340

GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
                345                 350

TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
    355                 360                 365

GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
            370                 375

CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
380                 385                 390

TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
        395                 400                 405

GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
Ala Asp Ser Ala Xaa Ser
                410 411

CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450

AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC 1550

TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650

TTGTTTTCAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAG 1750

GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 930 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
 1               5                  10

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
        15                  20                  25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met
                30                  35
```

```
GCC GAG GTG CAG CTG GTG CAG TCT GGG GGA GGT GTG GAA 153
Ala Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu
     40                  45                  50

CGG CCG GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192
Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
             55                  60

GGA TTC ACC TTT GAT GAT TAT GGC ATG AGC TGG GTC CGC 231
Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg
 65                  70                  75

CAA GCT CCA GGG AAG GGG CTG GAG TGG GTC TCT GGT ATT 270
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile
         80                  85                  90

AAT TGG AAT GGT GGT AGC ACA GGA TAT GCA GAC TCT GTG 309
Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val
                 95                 100

AAG GGC CGA GTC ACC ATC TCC AGA GAC AAC GCC AAG AAC 348
Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn
    105                 110                 115

TCC CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC 387
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            120                 125

ACG GCC GTA TAT TAC TGT GCG AAA ATC CTG GGT GCC GGA 426
Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala Gly
130                 135                 140

CGG GGC TGG TAC TTC GAT CTC TGG GGG AAG GGG ACC ACG 465
Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr
        145                 150                 155

GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA GGC GGA GGT 504
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
                160                 165

GGC AGC GGC GGT GGC GGA TCG TCT GAG CTG ACT CAG GAC 543
Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln Asp
    170                 175                 180

CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA GTC AGG ATC 582
Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile
            185                 190

ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA AGC 621
Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
195                 200                 205

TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC 660
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val
        210                 215                 220

ATC TAT GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC 699
Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp
                225                 230
```

```
CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA GCT TCC TTG 738
Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu
    235                 240                 245

ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG GCT GAC TAT 777
Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr
            250                 255

TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC CAT GTG GTA 816
Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val
260                 265                 270

TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT GCG GCC 855
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
        275                 280                 285

GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA AAA 894
Ala His His His His His His Gly Ala Ala Glu Gln Lys
                290                 295

CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA TAG 930
Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
    300                 305             309
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 939 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
  1               5                  10

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
        15                  20                  25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met
                30                  35

GCC GGG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTC 153
Ala Gly Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
    40                  45                  50

CAG CCT GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192
Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
            55                  60

GGA TTC ACC TTT AGT AGC TAT TGG ATG AGC TGG GTC CGC 231
Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg
 65                  70                  75
```

```
CAG GCT CCA GGG AAG GGG CTG GAG TGG GTG GCC AAC ATA 270
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile
         80                  85                  90

AAG CAA GAT GGA AGT GAG AAA TAC TAT GTG GAC TCT GTG 309
Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
                95                 100

AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC 348
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
    105                 110                 115

TCA CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC 387
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            120                 125

ACG GCT GTG TAT TAC TGT GCG AGA GAT CTT TTA AAG GTC 426
Thr Ala Val Tyr Tyr Cys Ala Arg Asp Leu Leu Lys Val
130                 135                 140

AAG GGC AGC TCG TCT GGG TGG TTC GAC CCC TGG GGG AGA 465
Lys Gly Ser Ser Ser Gly Trp Phe Asp Pro Trp Gly Arg
        145                 150                 155

GGG ACC ACG GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA 504
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
                160                 165

GGC GGA GGT GGT AGC GGC GGT GGC GGA TCG TCT GAG CTG 543
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu
    170                 175                 180

ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA 582
Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr
            185                 190

GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT 621
Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr
195                 200                 205

TAT GCA AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT 660
Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
        210                 215                 220

GTA CTT GTC ATC TAT GGT AAA AAC AAC CGG CCC TCA GGG 699
Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly
                225                 230

ATC CCA GAC CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA 738
Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr
    235                 240                 245

GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG 777
Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu
            250                 255

GCT GAC TAT TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC 816
Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn
260                 265                 270
```

```
CAT GTG GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA 855
His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
        275                 280                 285

GGT GCG GCC GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA 894
Gly Ala Ala Ala His His His His His His Gly Ala Ala
                290                 295

GAA CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC 933
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala
    300                 305                 310

GCA TAG 939
Ala
312
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 933 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
  1               5                  10

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
          15                  20                  25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met
                  30                  35

GCC CAG GTG CAG CTG GTG CAG TCT GGG GGA GGC GTG GTC 153
Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val
       40                  45                  50

CAG CCT GGG CGG TCC CTG AGA CTC TCC TGT GCA GCT TCT 192
Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
              55                  60

GGG TTC ATT TTC AGT AGT TAT GGG ATG CAC TGG GTC CGC 231
Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp Val Arg
  65                  70                  75

CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCA GGT ATT 270
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile
          80                  85                  90

TTT TAT GAT GGA GGT AAT AAA TAC TAT GCA GAC TCC GTG 309
Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val
                  95                  100
```

```
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC 348
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
    105                 110                 115

ACG CTG TAT CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC 387
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            120                 125

ACG GCT GTG TAT TAC TGT GCG AGA GAT AGG GGC TAC TAC 426
Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Tyr Tyr
130                 135                 140

TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC 465
Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val
        145                 150                 155

TCC TCA GGT GGA GGC GGT TCA GGC GGA GGT GGC TCT GGC 504
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                160                 165

GGT GGC GGA TCG CAG TCT GTG TTG ACG CAG CCG CCC TCA 543
Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser
    170                 175                 180

GTG TCT GGG GCC CCA GGA CAG AGG GTC ACC ATC TCC TGC 582
Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys
            185                 190

ACT GGG AGA AGC TCC AAC ATC GGG GCA GGT CAT GAT GTA 621
Thr Gly Arg Ser Ser Asn Ile Gly Ala Gly His Asp Val
195                 200                 205

CAC TGG TAC CAG CAA CTT CCA GGA ACA GCC CCC AAA CTC 660
His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        210                 215                 220

CTC ATC TAT GAT GAC AGC AAT CGG CCC TCA GGG GTC CCT 699
Leu Ile Tyr Asp Asp Ser Asn Arg Pro Ser Gly Val Pro
                225                 230

GAC CGA TTC TCT GGC TCC AGG TCT GGC ACC TCA GCC TCC 738
Asp Arg Phe Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser
    235                 240                 245

CTG GCC ATC ACT GGG CTC CAG GCT GAA GAT GAG GCT GAT 777
Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp
            250                 255

TAT TAC TGC CAG TCC TAT GAC AGC AGC CTG AGG GGT TCG 816
Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Arg Gly Ser
260                 265                 270

GTA TTC GGC GGA GGG ACC AAG GTC ACT GTC CTA GGT GCG 855
Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala
        275                 280                 285

GCC GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA 894
Ala Ala His His His His His His Gly Ala Ala Glu Gln
                290                 295
```

```
AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA  930
Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
    300                 305                 310
```

TAG 933

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile
 1               5                  10                  15

Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro
            20                  25                  30

Phe Tyr Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu Val Gln
            35                  40                  45

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser
            50                  55                  60

Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp
            65                  70                  75

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile
            80                  85                  90

Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly
            95                 100                 105

Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
           110                 115                 120

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
           125                 130                 135

Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp
           140                 145                 150

Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
           155                 160                 165

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln
           170                 175                 180

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr
           185                 190                 195

Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln
           200                 205                 210

Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn
           215                 220                 225
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Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser
230 235 240

Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp
245 250 255

Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
260 265 270

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
275 280 285

Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
290 295 300

Ser Glu Glu Asp Leu Asn Gly Ala Ala
305 309

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile
1 5 10 15

Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro
20 25 30

Phe Tyr Ala Ala Gln Pro Ala Met Ala Gly Val Gln Leu Val Glu
35 40 45

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
50 55 60

Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp
65 70 75

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile
80 85 90

Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly
95 100 105

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
110 115 120

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
125 130 135

Ala Arg Asp Leu Leu Lys Val Lys Gly Ser Ser Ser Gly Trp Phe
140 145 150

Asp Pro Trp Gly Arg Gly Thr Thr Val Thr Val Ser Ser Gly Gly
155 160 165

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu
170 175 180

Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val
185 190 195

Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
200 205 210

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
215 220 225

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly
230 235 240

Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln
245 250 255

Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser
260 265 270

Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
275 280 285

Gly Ala Ala Ala His His His His His His Gly Ala Ala Glu Gln
290 295 300

Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
305 310 312

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile
1 5 10 15

Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro
20 25 30

Phe Tyr Ala Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln
35 40 45

Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser
50 55 60

Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp
65 70 75

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile
80 85 90

Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly
95 100 105

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
110 115 120

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
125 130 135

Ala Arg Asp Arg Gly Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly
140 145 150

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
155 160 165

Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro
170 175 180

Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
185 190 195

Gly Arg Ser Ser Asn Ile Gly Ala Gly His Asp Val His Trp Tyr
200 205 210

Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asp
215 220 225

Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Arg
230 235 240

Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu
245 250 255

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Arg
260 265 270

Gly Ser Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala
275 280 285

Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu
290 295 300

Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
305 310

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGCGGATAAC AATTTCACAC AGG 23

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGTCTTTC CAGACGGTAG T 21

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu
1 5 10 12